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WIPREH (TM)

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Release 3.1A John F. Collins, Biocomputing Research Unit.  
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MPSrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm  
Run on: Thu May 6 15:08:47 1999; MagPar time 1644.23 Seconds  
Tabular output not generated.

Title: >US-09-037-460-1  
Description: (1-1271) from US09037460.seq  
Perfect Score: 1266  
N.A. Sequence: 1 CTGCTTCCACGACGAAAGA.....GTNCCCTNTCTNAAGGAC 1271  
Comp: GACGAAGGTGGTCGTCTT.....CAANGGANAGANTTCTTG

Scoring table: TABLE default  
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 2275026 seqs, 895388244 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: emb1-est56  
Database: genbank-est109  
1:em\_est1 2:em\_gss1 3:em\_gss2 4:em\_gss3  
5:gb\_est1 6:gb\_est10 7:gb\_est11 8:gb\_est12 9:gb\_est13  
10:gb\_est14 11:gb\_est15 12:gb\_est16 13:gb\_est17  
14:gb\_est18 15:gb\_est19 16:gb\_est2 17:gb\_est20  
18:gb\_est21 19:gb\_est3 20:gb\_est4 21:gb\_est5 22:gb\_est6  
23:gb\_est7 24:gb\_est8 25:gb\_est9 26:gb\_gss1 27:gb\_gss2  
28:gb\_gss3 29:gb\_gss4

Statistics: Mean 11.873; Variance 3.231; scale 3.674

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description            | Pred. No. |
|------------|-------|-------------|--------|----|------------------------|-----------|
| 1          | 412   | 32.5        | 425    | 21 | W46667                 | 0.00e+00  |
| 2          | 139   | 11.0        | 351    | 24 | AA296697               | 1.44e-152 |
| 3          | 62    | 4.9         | 252    | 12 | ESR112419 Aorta endoth | 1.37e-44  |
| 4          | 56    | 4.4         | 252    | 12 | AA754459               | 5.86e-37  |
| 5          | 48    | 3.8         | 247    | 12 | AA754458               | 5.86e-37  |
| 6          | 46    | 3.6         | 247    | 12 | AA754458               | 5.86e-37  |
| 7          | 35    | 2.8         | 2275   | 11 | AF034173               | 5.24e-12  |
| 8          | 33    | 2.6         | 236    | 11 | AA702386               | 5.24e-12  |
| 9          | 30    | 2.4         | 467    | 29 | AQ151727               | 6.83e-10  |
| 10         | 29    | 2.3         | 199    | 14 | AA926494               | 7.59e-07  |
| 11         | 29    | 2.3         | 265    | 15 | AI005619               | 7.20e-06  |
| 12         | 29    | 2.3         | 284    | 14 | AA890895               | 7.20e-06  |
| 13         | 29    | 2.3         | 369    | 10 | AA642307               | 7.20e-06  |

|    |     |     |    |            |                        |          |
|----|-----|-----|----|------------|------------------------|----------|
| 14 | 2.3 | 369 | 11 | AA670056   | ag39h07.s1 Jia bone ma | 7.20e-06 |
| 15 | 2.3 | 379 | 10 | AA620322   | af09g06.s1 Soares test | 7.20e-06 |
| 16 | 2.3 | 399 | 17 | AI038446   | ow21d11.x1 Soares para | 7.20e-06 |
| 17 | 2.3 | 420 | 8  | AA397891   | zt86c04.r1 Soares test | 7.20e-06 |
| 18 | 2.3 | 421 | 8  | AA494213   | ng99g03.s1 NCI_CGAP.Th | 7.20e-06 |
| 19 | 2.3 | 433 | 15 | AI003780   | ou91g01.x1 NCI_CGAP_Ki | 7.20e-06 |
| 20 | 2.3 | 441 | 19 | N72081     | yz97d02.s1 Homo sapien | 7.20e-06 |
| 21 | 2.3 | 451 | 8  | AA126449   | zn85e12.s1 Strategene  | 7.20e-06 |
| 22 | 2.3 | 469 | 6  | CU5912     | similar to none, mRNA  | 7.20e-06 |
| 23 | 2.3 | 499 | 15 | AA041163   | ov59g09.x1 Soares test | 7.20e-06 |
| 24 | 2.3 | 555 | 20 | AA001197   | ze48e12.s1 Soares reti | 7.20e-06 |
| 25 | 2.3 | 719 | 14 | AA950736   | LD30843.5prime LD Dros | 7.20e-06 |
| 26 | 2.2 | 275 | 12 | AA789162   | ag58a11.s1 Gessler Wil | 6.51e-05 |
| 27 | 2.2 | 280 | 13 | AA830387   | oc44h08.s1 NCI_CGAP_GC | 6.51e-05 |
| 28 | 2.2 | 332 | 11 | AA580607   | nc80b11.s1 NCI_CGAP_GC | 6.51e-05 |
| 29 | 2.2 | 343 | 11 | AA719452   | zh35h07.s1 Soares pine | 6.51e-05 |
| 30 | 2.2 | 356 | 7  | HUM215G05B | Human aorta cDNA 5'-en | 6.51e-05 |
| 31 | 2.2 | 361 | 8  | AA233919   | zr49e02.s1 Soares NHM  | 6.51e-05 |
| 32 | 2.2 | 364 | 13 | AA804446   | nz38c06.s1 NCI_CGAP_GC | 6.51e-05 |
| 33 | 2.2 | 375 | 15 | AI049727   | an37c10.x1 Gessler Wil | 6.51e-05 |
| 34 | 2.2 | 409 | 10 | AA653384   | ag55h03.s1 Gessler Wil | 6.51e-05 |
| 35 | 2.2 | 416 | 21 | W65422     | z33b05.s1 Soares testa | 6.51e-05 |
| 36 | 2.2 | 426 | 10 | AA625676   | zu86a05.s1 Soares feta | 6.51e-05 |
| 37 | 2.2 | 430 | 11 | AA662165   | ns66c08.s1 NCI_CGAP_Pr | 6.51e-05 |
| 38 | 2.2 | 430 | 10 | AA614832   | nn96c07.s1 NCI_CGAP_Br | 6.51e-05 |
| 39 | 2.2 | 437 | 8  | AA234168   | zr49e02.s1 Soares NHM  | 6.51e-05 |
| 40 | 2.2 | 441 | 19 | H92123     | ys84h01.r1 Homo sapien | 6.51e-05 |
| 41 | 2.2 | 441 | 14 | AA902495   | ok91h09.s1 NCI_CGAP_Lu | 6.51e-05 |
| 42 | 2.2 | 496 | 13 | AA868954   | ak55e05.s1 Soares test | 6.51e-05 |
| 43 | 2.2 | 522 | 22 | AA204900   | zg61a09.r1 Strategene  | 6.51e-05 |
| 44 | 2.2 | 614 | 14 | AA898668   | NCM7G1T7 Mycelial Neur | 6.51e-05 |
| 45 | 2.2 | 748 | 15 | C93732     | Dictyostellum discoide | 6.51e-05 |

ALIGNMENTS

| RESULT     | 1 | W46667   | 425 bp | mRNA | EST | 11-OCT-1996 |
|------------|---|--|--------|------|-----|-------------|
| LOCUS      |   | zc33e02.r1 Soares senescent fibroblasts NbHSF Homo sapiens CDNA  |        |      |     |             |
| DEFINITION |   | clone 324122 5', mRNA sequence.  |        |      |     |             |
| ACCESSION  |   | W46667   |        |      |     |             |
| NID        |   | 91331295   |        |      |     |             |
| KEYWORDS   |   | EST.   |        |      |     |             |
| SOURCE     |   | human.   |        |      |     |             |
| ORGANISM   |   | Homo sapiens   |        |      |     |             |
| REFERENCE  |   | Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homiidae; Homo.   |        |      |     |             |
| AUTHORS    |   | 1 (bases 1 to 425)<br>Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.   |        |      |     |             |
| TITLE      |   | The WashU-Merck EST Project  |        |      |     |             |
| JOURNAL    |   | Unpublished (1995)   |        |      |     |             |
| COMMENT    |   | Contact: Wilson RK<br>WashU-Merck EST Project<br>Washington University School of Medicine<br>4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108<br>Tel: 314 286 1800<br>Fax: 314 286 1810<br>Email: est@wustl.edu<br>This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.<br>Insert Length: 1322 Std Error: 0.00<br>Seq primer: mob.REGA-ET<br>High quality sequence stop: 395.<br>Location/Qualifiers<br>1. .425<br>/organism="Homo sapiens"<br>/note="Vector: pT73D (Pharmacia) with a modified polylinker V_Type: phagemid; Site_1: Not I; Site_2: Eco |        |      |     |             |

FEATURES  
Source

RI: TGTTACCAATCTGAAGTGGAGCGCGCATTTTTTTTTTTTTTTTTTTT  
 3'], double-stranded cDNA was size selected, ligated to  
 Eco RI adapters (Pharmacia), digested with Not I and  
 cloned into the Not I and Eco RI sites of a modified pT713  
 vector (Pharmacia). Library went through one round of  
 normalization to a Cot = 5. Library constructed by Bento  
 Soares and M. Fatima Bonaldo.  
 /db\_xref="taxon:9606"  
 /clone="324122"  
 /clone.lib="Soares senescent fibroblasts NBHSF"  
 /tissue.type="senescent fibroblast"  
 /lab\_host="DH10B (ampicillin resistant)"  
 <1. >425

BASE COUNT 144 a 50 c 102 g 126 t 3 others  
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 Query Match 32.5%; Score 412; DB 21; Length 425;  
 Best Local Similarity 98.1%; Pred. No. 0.00e+00;  
 Matches 417; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

Db 1 GTTAAATATTCGAATGATGATGATTTTAAATGTTGTGTATAGTAACTAGGAAC 60  
 Qy 812 GTTAAATATTCGAATGATGATGATTTTAAATGTTGTGTATAGTAACTAGGAAC 871  
 Db 61 TAAAAATGCAATTTAGTAACTTTACATGGAGACAGTCAACCAAGAGGAGCTAGGCA 120  
 Qy 872 TAAAAATGCAATTTAGTAACTTTACATGGAGACAGTCAACCAAGAGGAGCTAGGCA 931  
 Db 121 AAGCTGAAGACCGCAGTCAGTCAATAGTTCTTTGACTTTGATGTACATTAATGTTGGG 180  
 Qy 932 AAGCTGAAGACCGCAGTCAGTCAATAGTTCTTTGACTTTGATGTACATTAATGTTGGG 991  
 Db 181 ATATGGAATGAGACTTAAGACGAGGAGATGCGNNAGGGGTGGGAGTGGGAATAAAA 240  
 Qy 992 ATATGGAATGAGACTTAAGACGAGGAGATGCGNNAGGGGTGGGAGTGGGAATAAAA 1051  
 Db 241 ATATTTAGCCCTCTCTGTTAGTGGTCTCTAGATTTAAATATGCTTTTTTTTTTTT 300  
 Qy 1052 ATATTTAGCCCTCTCTGTTAGTGGTCTCTAGATTTAAATATGCTTTTTTTTTTTT 1111  
 Db 301 TTTTGGCTTTGGGAAAGTCAAAATTAACCAACCAAGGAGGAGTGAAGA 360  
 Qy 1112 TTTTGGCTTTGGGAAAGTCAAAATTAACCAACCAAGGAGGAGTGAAGA 1170  
 Db 361 TGTTGAGCTTTATGAAATTTAGTAACTAAACAGCTTTGAAGTGAAGCAATTTCAAAA 420  
 Qy 1171 TGTTGAGCTTTATGAAATTTAGTAACTAAACAGCTTTGAAGTGAAGCAATTTCAAAA 1230  
 Db 421 GGCTG 425  
 Qy 1231 GGCTG 1235

RESULT 2 AA296697 351 bp mRNA EST 18-APR-1997  
 LOCUS EST112419 Aorta endothelial cells, TNF alpha-treated Homo sapiens  
 DEFINITION CDNA 5' end similar to endothelial cell-specific secretory  
 molecule, mRNA sequence.  
 ACCESSION AA296697  
 NID 91949189  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;  
 Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;  
 Homo.  
 1 (bases 1 to 351)  
 AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,  
 Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,  
 White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Whai,C.,  
 Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,  
 Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,  
 Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,

Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,  
 Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,  
 Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,  
 Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,  
 Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,  
 Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,  
 He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,  
 Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H.,  
 Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,  
 Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,  
 Fraser,C.M. and Venter,J.C.

Initial assessment of human gene diversity and expression patterns  
 based upon 83 million nucleotides of cDNA sequence  
 Nature 377 (6547 Suppl), 3-174 (1995)  
 96026280  
 Other\_ESTs: THCL54673  
 Contact: Kerlavage, AR  
 Bioinformatics  
 The Institute for Genomic Research  
 9712 Medical Center Drive, Rockville, MD 20850 USA  
 Tel: 3018699056  
 Fax: 3018699423  
 Email: arkerlavet@tigr.org

For clone availability, additional sequence and expression  
 information related to this EST, please check the TIGR Human Gene  
 Index (<http://www.tigr.org/tdb/hgi/hgi.html>)  
 Seq primer: M13 Reverse.

FEATURES  
 source Location/Qualifiers  
 1..351  
 /organism="Homo sapiens"  
 /note="Organ: aorta; Vector: pBluescript SK-; Site\_1:  
 EcoRI; Site\_2: XhoI"  
 /db\_xref="AACC (inhost):115698"  
 /clone\_lib="Aorta endothelial cells, TNF alpha-treated"  
 /cell\_type="endothelial cell"  
 /dev\_stage="adult"  
 <1..>351  
 mrna  
 BASE COUNT 118 a 57 c 72 g 102 t 2 others  
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Query Match 11.0%; Score 139; DB 24; Length 351;  
 Best Local Similarity 94.0%; Pred. No. 1.44e-152;  
 Matches 140; Conservative 1; Mismatches 8; Indels 0; Gaps 0;  
 Db 1 GGGAAAGTCAAAATTAACACACCAAGAAACCCCTGAAGAAAGTGAAGCTT 60  
 Qy 1123 GGGAAAGTCAAAATTAACACACCAAGAAACCCCTGAAGAAAGTGAAGCTT 1182  
 Db 61 ATGGAAATTTGAGTAAACACACAGCTTTGACTGAGAGCAATTTCAAAGCGTGTGATCT 120  
 Qy 1183 ATGGAAATTTGAGTAAACACACAGCTTTGACTGAGAGCAATTTCAAAGCGTGTGATCT 1242  
 Db 121 AGTTCGCGGTTACCTGTATCTGAAGGAC 149  
 Qy 1243 AGCCCGCGGTTNCTNTNCTNAGGAC 1271

RESULT 3  
 LOCUS AA754459 252 bp mRNA EST 20-JAN-1998  
 DEFINITION 97SN1787 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa  
 ACCESSION AA754459  
 NID 92801165  
 KEYWORDS EST.  
 SOURCE rice.  
 ORGANISM Oryza sativa  
 Eukaryotes; Viridiplantae; Charophyta/Embryophyta group;  
 Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;  
 Poales; Poaceae; Oryza.  
 1 (bases 1 to 252)  
 REFERENCE Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R., Moon,E.P.,  
 Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,







[illegible]

SOURCE  
ORGANISM Homo sapiens  
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 369)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Unknown library type  
Seq primer: -40m13 fwd. ET from Amersham  
High quality sequence stop: 328.  
Location/Qualifiers  
1. .369  
/organism="Homo sapiens"  
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
was prepared from human tonsillar cells enriched for  
germinal center B cells by flow sorting (CD20+, IgD-),  
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman  
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was  
primed with a Not I - oligo(dT) primer.  
[5'-TGTTACCAATCTGAAGTGGAGCGCGCCCTCATTTTTTTTTTTT-  
3']. Double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT7T3 vector. Library  
went through one round of normalization, and was  
constructed by Bento Soares and M. Fatima Bonaldo."  
/db\_xref="taxon:9606"  
/clone="IMAGE:1184639"  
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/tissue\_type="germinal center B cell"  
/lab\_host="DH10B"  
BASE COUNT 119 a 86 c 72 g 92 t  
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Best Local Similarity 82.2%; Pred. No. 7.20e-06;  
Matches 37; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
Db 21 TTTTGTGCTTTTGGGCTTTGGGAAAGTCAAAATAAACAA 1144  
|||||  
QY 1100 TTTTGTGCTTTTGGGCTTTGGGAAAGTCAAAATAAACAA 1144  
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RESULT 14  
LOCUS AA670056 369 bp mRNA EST 20-NOV-1997  
DEFINITION ag39h07.s1 Jia bone marrow stroma Homo sapiens cDNA clone 1119229  
3', mRNA sequence.  
ACCESSION AA670056  
NID 92631555  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 369)  
AUTHORS Jia, L., Wilkin, D., Bittner, M., Robey, P., Young, M., Yamada, Y.,  
Krizman, D., Liotta, L., Bonner, R., Schuler, G., Boguski, M.,  
Powell, J., Lennon, G., Roadman, D., Hotchkiss, R., Meitzer, P.,  
Trent, J., Hillier, L., Allen, M., Bowles, L., Geisel, S., Kucaba, T.,  
Marra, M., Martin, J., Steptoe, M., Tan, F., Theising, B., Bowers, Y.,  
Wyllie, T., Waterston, R., Wilson, R. and Francomano, C.  
WashU-MGB/NHGRI EST Project  
Unpublished (1997)  
TITLE Contact: Wilton RK / Jia L  
JOURNAL WashU-MGB/NHGRI EST Project  
COMMENT Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium ([infoimage.llnl.gov](http://infoimage.llnl.gov)) for further information.  
Seq primer: -40m13 fwd. ET from Amersham  
High quality sequence stop: 336.  
Location/Qualifiers  
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/organism="Homo sapiens"  
/note="Vector: pBluescript; Site 1: EcoRI; Site 2: XhoI;  
mRNA made from human bone marrow stroma, cDNA made by  
oligo-dT priming. Directionally cloned. Size-selected for  
average insert size >0.5 kb. Library supplied by Dr. Libin  
Jia (NHGRI)."  
/db\_xref="taxon:9606"  
/clone="1119229"  
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/sex="mixed"  
/tissue\_type="bone marrow stroma"  
/dev\_stage="mixed"  
/lab\_host="XLI-Blue MRF"/SOLR"  
BASE COUNT 140 a 69 c 50 g 110 t  
ORIGIN  
Query Match 2.3%; Score 29; DB 11; Length 369;  
Best Local Similarity 78.7%; Pred. No. 7.20e-06;  
Matches 37; Conservative 1; Mismatches 9; Indels 0; Gaps 0;  
Db 250 TTTTCCCTTCGAAATCCCAAAAAAAGACACAGTAA 296  
|||||  
Cp 1136 TTTTGACTTTTCCCAAGCCCAAAAAAAGACATATTAA 1090  
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RESULT 15  
LOCUS AA620322 379 bp mRNA EST 14-OCT-1997  
DEFINITION af06g06.s1 Soares testis NHT Homo sapiens cDNA clone 1030906 3',  
mRNA sequence.  
ACCESSION AA620322  
NID 92524261  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 379)  
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,  
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,  
Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,  
Theising, B., White, Y., Wyllie, T., Waterston, R. and Wilson, R.  
WashU-NCI human EST Project  
Unpublished (1997)  
TITLE Contact: Wilton RK  
JOURNAL Washington University School of Medicine  
COMMENT 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium ([infoimage.llnl.gov](http://infoimage.llnl.gov)) for further information.  
Seq primer: -40m13 fwd. ET from Amersham  
High quality sequence stop: 371.  
Location/Qualifiers  
1. .379  
/organism="Homo sapiens"  
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
was prepared from mRNA obtained from Clontech  
Laboratories, Inc., and primed with a Not I - oligo(dT)  
primer [5',  
TGTTACCAATCTGAAGTGGAGCGCGCCCAATTTTTTTTTTTT 3'].

Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo." /db\_xref="taxon:9606"

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/db_xref="taxon:9606"
/clone="1039906"
/clone_lib="Soares testis NHT"
/sex="male"
/lab_host="DH10B"
71 c 50 g 115 t

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| BASE COUNT | 143 a | 71 c | 50 g | 115 t |
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| ORIGIN     |       |      |      |       |

Query Match 2.3%; Score 29; DB 10; Length 379;  
Best Local Similarity 78.7%;  
Pred. NO. 7.20e-06;  
Matches 37; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Db 257 TTTTGCCCTTGCAAGATCCAAAAAAGCAACAGTAA 303  
||||| | | | | | | | | | | | | | | | | | | | |  
Cp 1136 TTTTGACTTTTCCCAAGCCCAAAAAAAGCAIYATTA 1090

Search completed: Thu May 6 16:02:01 1999  
Job time : 3194 secs.